ABSTRACT

The present invention concerns a method for determining at least one functional SNP in a gene, comprising preselecting a candidate gene, providing a sample population comprising a significant number of individuals chosen substantially at random from the general population, isolating from each individual of the sample population at least one fragment of the nucleotide sequence of the preselected candidate gene, identifying at least one SNP in at least one fragment and determining the functionality of said SNP(s). The present invention also concerns applications of this method.